

## SEQUENCE LISTING

<110> DeveloGen Aktiengesellschaft für entwicklungsbiolo

<120> Method for preventing and treating diabetes using DG119

<130> 32043PWO

<140> PCT/EP2004/013535

<141> 2004-11-29

<150> EP03/027514.3

<151> 2003-11-28

<160> 9

<170> PatentIn Ver. 2.1

<210> 1

<211> 719

<212> PRT

<213> zebrafish

<220>

<223> DG119-1A1A

<400> 1

Met Thr Glu Met Lys Ile Trp Cys Val Leu Leu Met Ala Phe Ala Leu  
1 5 10 15

Thr Ser Ala Ala Pro Lys Ser His Leu Arg Leu Glu Glu Lys Thr Lys  
20 25 30

Asp Asn Asn Asp Thr Leu Gln Val Glu Ile Asp Asn Gln Glu His Ile  
35 40 45

Leu Ser Gln Leu Leu Gly Asp Tyr Asp Lys Val Lys Ala Leu Ser Glu  
50 55 60

Gly Ser Asp Cys Gly Cys Lys Cys Val Val Arg Pro Leu Ser Ala Ser  
65 70 75 80

Ala Cys Gln Arg Ile Arg Glu Gly His Ala Thr Pro Gln Asp Phe Tyr  
85 90 95

Thr Val Glu Thr Ile Thr Ser Gly Pro His Cys Lys Cys Ala Cys Ile  
100 105 110

Ala Pro Pro Ser Ala Leu Asn Pro Cys Glu Gly Asp Phe Arg Leu Lys  
115 120 125

Lys Leu Arg Gln Ala Gly Lys Asp Asn Ile Lys Leu Ser Thr Ile Leu  
130 135 140

Glu Leu Leu Glu Gly Ser Phe Tyr Gly Met Asp Leu Leu Lys Leu His  
145 150 155 160

Ser Val Thr Thr Lys Ile Leu Asp Arg Met Asp Thr Ile Glu Lys Met  
165 170 175

Val Leu Asn Asn Gln Thr Glu Glu Lys Leu Asn Thr Ile Ser Thr Ser  
180 185 190

Pro Asn Pro Gln Leu Ser Thr Ser Ser Pro Thr Thr Leu Pro Ser Val  
195 200 205

Ile Gln Glu Lys Ser Thr Ser Leu Arg Gln Gln Asn Asp Glu Ala Ala  
210 215 220

Ala Phe Gln His Met Glu Ser Lys Tyr Glu Glu Lys Phe Val Gly Asp  
225 230 235 240

Ile Leu Asn Ser Gly Ser Asp Leu Asn Lys Ala Thr Thr Ala Leu Gln  
245 250 255

Glu Gln Glu Gln Gln Gly Arg Lys Lys Gln Pro Lys Ile Thr Val Arg  
260 265 270

Gly Ile Thr Tyr Tyr Arg Ser Asp Pro Val Asp Glu Met Asp Ser Glu  
275 280 285

Lys Asn Leu Lys Glu Thr Ser Ala Ser Ser Val Thr Gln Thr Gly Ala  
290 295 300

Leu Ile Lys Glu His Leu Lys Ala Ser Thr Gln Ser Thr Leu Asn Thr  
305 310 315 320

Leu Thr Pro Ser Pro Thr Ser His Ser Asn Ala Leu Thr Val Thr Glu  
325 330 335

Ser Ser Val Gly Ile Asn Ala His Lys Gly Glu Val Thr Thr Ile Val  
340 345 350

Met Thr Ala Ser Val Thr Gly Ser Lys Thr Asp Ser Val Thr Asp Leu  
355 360 365

Thr Gln Leu Ser Pro Arg Val Arg Glu Thr Leu Thr Thr Thr Arg Thr  
370 375 380

Thr Thr Lys Thr Ala Thr Thr Ser Gln Pro Val Lys Arg Lys Tyr Ser  
385 390 395 400

Ile Ser Trp Asp Glu Glu Glu Ala Val Val Pro Glu Gln Val Glu  
405 410 415

Glu Glu Lys Ala Val Lys Pro Val Val Glu Asp Lys Val Gly Glu Glu  
420 425 430

Pro Gln Arg Lys Pro Gly Thr Ala His His Gln Ala Lys Thr Ile Ser  
435 440 445

Thr Val Lys Gln Gln Ile Lys Phe Ser Leu Gly Met Cys Lys Asp Thr  
450 455 460

Leu Ala Thr Ile Ser Glu Pro Ile Thr His Asn Thr Tyr Gly Arg Asn  
465 470 475 480

Glu Gly Ala Trp Met Lys Asp Pro Leu Asp Gln Asp Asp Lys Ile Tyr  
485 490 495

Val Thr Asn Tyr Tyr Gly Asn Asn Leu Leu Glu Phe Arg Asn Ile  
500 505 510

Asp Val Phe Lys Gln Gly Arg Phe Thr Asn Ser Tyr Lys Leu Pro Tyr  
515 520 525

Asn Trp Ile Gly Thr Gly His Val Val Tyr Lys Gly Ala Phe Tyr Tyr  
530 535 540

Asn Arg Ala Phe Ser Arg Asp Ile Ile Lys Phe Asp Leu Arg Leu Arg  
545 550 555 560

Tyr Val Ala Ala Trp Thr Met Leu His Asp Ala Val Phe Glu Asn Asp  
565 570 575

Asp Val Ser Ser Trp Arg Trp Arg Gly Asn Ser Asp Met Asp Leu Ala  
580 585 590

Ile Asp Glu Ser Gly Leu Trp Val Ile Tyr Pro Ala Leu Asp Asp Glu  
595 600 605

Gly Phe Leu Gln Glu Val Ile Val Leu Ser Arg Leu Asn Pro Thr Asp  
610 615 620

Leu Ser Met Lys Arg Glu Thr Thr Trp Arg Thr Gly Leu Arg Arg Asn  
625 630 635 640

Arg Tyr Gly Asn Cys Phe Ile Val Cys Gly Val Leu Tyr Ala Thr Asp  
645 650 655

Ser Tyr Asn Gln Gln Asp Thr Asn Leu Ser Tyr Ala Phe Asp Thr His  
660 665 670

Thr Asn Thr Gln Val Ile Pro His Leu Pro Phe Ser Asn Asn Tyr Thr  
675 680 685

Tyr Val Thr Gln Ile Asp Tyr Asn Pro Lys Glu Arg Val Leu Tyr Ala  
690 695 700

Trp Asp Asn Gly His Gln Val Thr Tyr Asn Val Gln Phe Ala Tyr  
705 710 715

<210> 2

<211> 594

<212> PRT

<213> zebrafish

<220>

<223> DG119-1B1B

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Met Gly Leu Leu Leu Tyr Ile Phe Cys Cys Val Phe Cys Leu Thr Arg  
1 5 10 15

Ala Asn Val Glu Gln Gln Ala Thr Asp Asn Thr Asp Asn Arg Ala Thr  
20 25 30

Leu Glu Asp Glu Met Asp Asn Gln Glu Asn Ile Leu Thr Gln Leu Ile  
35 40 45

Gly Asp Tyr Asp Lys Val Lys Thr Leu Ser Glu Gly Ser Asp Cys Gln  
50 55 60

Cys Lys Cys Val Val Arg Pro Met Ser Arg Ser Ala Cys Lys Arg Ile  
65 70 75 80

Glu Glu Ala Gln Ala Lys Ile Glu Asp Phe Tyr Thr Val Glu Pro Val  
85 90 95

Thr Ala Gly Pro Asn Cys Lys Cys Ala Cys Ile Ala Pro Pro Ser

100	105	110
Ala Leu Asn Pro Cys Glu Gly Asp Phe Arg Phe Lys Lys Leu Gln Lys		
115	120	125
Thr Gly Gln Tyr Asp Ile Lys Leu Ser Asn Ile Met Asp Leu Leu Glu		
130	135	140
Glu Arg Val Asp Asn Ile Glu Lys Gly Glu Lys Gly Gln Gly Lys Gly		
145	150	155
Ala Arg Ser Asn Gln Arg Gln Glu Lys Lys Arg Leu Ser Val Val		
165	170	175
Cys Trp Ser Leu His Cys Arg Arg Thr Gln Gln Arg Leu Leu Leu Thr		
180	185	190
Leu Arg Tyr Arg Cys Xaa Ser Val Leu Glu Pro Ser Leu Gln Lys Asn		
195	200	205
Ala Ala Ala Ala Phe Ala His Thr Glu Val Gln Met Gln Gln Phe Ile		
210	215	220
Pro Asp Gln Arg Lys Tyr Glu Glu Lys Phe Val Gly Asn Gln Gly Pro		
225	230	235
Ser Lys Pro Val Leu Lys Lys Ser Lys Ser Glu Gly Gln Glu Glu Gln		
245	250	255
His Lys Pro Ala Lys Thr Lys Ala Asp Ala Lys Asn Met Ser Leu Arg		
260	265	270
Ser Met Thr Phe Tyr Lys Ala Asn Arg Met Glu Asp Ser Glu Gly Glu		
275	280	285
Glu Arg Asp Leu Ile Ile Glu Asp Gln Leu His Lys Gln Gly Leu Asn		
290	295	300
Thr Pro Val Thr Pro Glu Ala Thr Val Thr Val Thr Gln Ser Thr		
305	310	315
320		
Thr Ile Asn Leu Asn Thr Gln Asn Phe Thr Thr Ala Arg Met Ser Asn		
325	330	335
Val Thr Lys Gln Thr Gln Gly Gln Ser Val Lys Ala Met Met Ser Ser		
340	345	350
Thr Ile Thr Thr Glu Arg Pro Thr Met Pro Thr Ser Thr Thr Ser Thr		

355	360	365
Ser Thr Met Thr Pro Gly Thr Asn Thr Thr Thr Ile Ala Thr Pro Leu		
370	375	380
Val Val Pro Lys Gln Leu Ala Ser Val Thr Val Gly Gln Val Ser Asn		
385	390	395
Ser Tyr Lys Leu Pro Tyr Asn Trp Ile Gly Thr Gly His Val Val Tyr		
405	410	415
Ser Gly Ser Phe Phe Tyr Asn Arg Ala Phe Ser Arg Asp Ile Ile Arg		
420	425	430
Phe Asp Leu Arg Leu Arg Tyr Val Ala Ala Trp Thr Thr Leu His Asp		
435	440	445
Ala Ile Leu Glu Glu Glu Ala Pro Trp Thr Trp Gly Gly His Ser		
450	455	460
Asp Ile Asp Phe Ser Val Asp Glu Ser Gly Leu Trp Leu Val Tyr Pro		
465	470	475
480		
Ala Leu Asp Asp Glu Gly Phe His Gln Glu Val Ile Ile Leu Ser Lys		
485	490	495
Leu Arg Ala Ser Asp Leu Gln Lys Glu Lys Ser Trp Arg Thr Gly Leu		
500	505	510
Arg Arg Asn Tyr Tyr Gly Asn Cys Phe Val Ile Cys Gly Val Leu Tyr		
515	520	525
Ala Val Asp Ser Phe Glu Arg Thr His Ala Asn Ile Ser Tyr Ala Phe		
530	535	540
Asp Thr His Thr His Thr Gln Met Ile Pro Arg Leu Pro Phe Ile Asn		
545	550	555
560		
Asn Tyr Thr Tyr Thr Thr Gln Ile Asp Tyr Asn Pro Lys Glu Arg Met		
565	570	575
Leu Tyr Ala Trp Asp Asn Gly His Gln Val Thr Tyr Asp Val Ile Phe		
580	585	590
Ala Tyr		

<210> 3  
<211> 146  
<212> PRT  
<213> zebrafish

<220>  
<223> DG119-2A2A

<400> 3  
Met Trp Arg Ile Val Glu Leu Val Ala Cys Leu Leu Met Met Ser Ser  
1 5 10 15  
  
His Val Ser Ser Gln Ser Lys Ile Phe Gly Glu Glu Gln Val Arg Met  
20 25 30  
  
Thr Ser Glu Gly Ser Asp Cys Arg Cys Lys Cys Ile Met Arg Pro Leu  
35 40 45  
  
Thr Arg Asp Ala Cys Ala Arg Leu Arg Thr Gly Ser Val Arg Val Glu  
50 55 60  
  
Asp Phe Tyr Thr Val Glu Thr Val Ser Ser Gly Ala Asp Cys Lys Cys  
65 70 75 80  
  
Ser Cys Thr Ala Pro Pro Ser Ser Leu Asn Pro Cys Glu Asn Glu Trp  
85 90 95  
  
Lys Arg Glu Lys Leu Lys Lys Gln Ala Pro Glu Leu Leu Lys Leu Gln  
100 105 110  
  
Ser Met Val Asp Leu Leu Glu Gly Thr Leu Phe Ser Met Asp Leu Leu  
115 120 125  
  
Lys Val His Ser Tyr Ile Asn Lys Val Val Ser Gln Met Asn Asn Leu  
130 135 140  
  
Glu Glu  
145

<210> 4  
<211> 287  
<212> PRT  
<213> zebrafish

<220>

<223> DG119-2B2B

<400> 4

Met	Trp	Ile	Tyr	Ala	Ser	Val	Leu	Thr	Tyr	Leu	Leu	Leu	Leu	Thr	Arg
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Asp	Ala	Arg	Ser	Leu	Ser	Lys	Ile	Phe	Gly	Glu	Pro	Glu	Pro	Val	Lys
			20					25						30	
Met	Ile	Ser	Glu	Gly	Ser	Asp	Cys	Arg	Cys	Lys	Cys	Val	Met	Arg	Pro
		35				40						45			
Leu	Ser	Ile	Glu	Ala	Cys	Ser	Arg	Leu	Arg	Asp	Gly	Ser	Leu	Arg	Val
		50			55				60						
Asp	Asp	Phe	Tyr	Thr	Val	Glu	Thr	Val	Ser	Ser	Gly	Ser	Asp	Cys	Lys
	65			70					75					80	
Cys	Ser	Cys	Thr	Ala	Pro	Pro	Ser	Ser	Leu	Asn	Pro	Cys	Glu	Asn	Glu
		85					90						95		
Trp	Arg	Thr	Glu	Lys	Leu	Xaa	Lys	Gln	Ala	Pro	Glu	Leu	Leu	Lys	Leu
		100					105					110			
His	Ser	Met	Val	Asp	Leu	Leu	Glu	Gly	Thr	Leu	Tyr	Ser	Met	Asp	Leu
		115				120					125				
Met	Lys	Val	His	Ala	Tyr	Met	Asn	Lys	Val	Val	Ser	Gln	Met	Asn	Thr
		130				135				140					
Leu	Glu	Glu	Val	Met	Thr	Ile	Lys	Thr	Asn	Leu	Thr	Arg	Glu	Asn	Glu
	145				150				155				160		
Phe	Val	Arg	Asp	Ser	Val	Val	Asn	Leu	Ser	Asn	Gln	Leu	Lys	Arg	Tyr
		165					170					175			
Glu	Asn	Tyr	Ser	Asp	Ile	Met	Val	Ser	Ile	Lys	Lys	Glu	Ile	Ser	Ser
		180					185					190			
Leu	Gly	Leu	Gln	Leu	Leu	Gln	Lys	Asp	Ala	Ala	Ser	Asp	Ser	Lys	Ala
		195				200					205				
Gln	Val	Gly	Thr	Glu	Ser	Lys	Lys	Ser	Lys	Glu	Ala	Ile	Lys	Pro	Pro
		210			215					220					
Asn	Lys	Lys	Pro	Pro	Ala	Val	Lys	Pro	Pro	Pro	Lys	Gln	Pro	Lys	Glu
		225				230			235			240			

Lys Pro Val Lys Pro Lys Lys Glu Ala Pro Ala Lys Ala Ala Lys Pro  
245 250 255

Ala Lys Pro Asp Pro Thr Thr Lys Thr Lys Thr Ser Val His Gln Thr  
260 265 270

Gly Val Ile Arg Gly Ile Thr Tyr Tyr Lys Ala Ser Lys Ser Glu  
275 280 285

<210> 5  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<223> m1192 forward primer

<400> 5  
gtgctgctgc tgctggttt g 21

<210> 6  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<223> m1192 reverse primer

<400> 6  
ctgtggctg gggtattctg c 21

<210> 7  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<223> mDG119-1 forward primer

<400> 7  
gaggaaaaatg acatagaaga gcagc

25

<210> 8  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<223> mDG119-1 reverse primer

<400> 8  
gctgatcttc tatcagcaag tccaa

24

<210> 9  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:probe

<220>  
<223> mDG119-1 probe

<400> 9  
cgatgagctt ttcaagtggcg acagtg

26